

Figure 1A

SEQ ID NO:18	-----	
SEQ ID NO:22	TKTSAPFLFTLSLRSNMTEERNVRKTRV-----VDVVLDVPIPIDDKDRDAVSQVC	
SEQ ID NO:20	MGGEAP-----EARRLDRAMSGGAGSIPEEALHLVLGYVDDPRDREAVSLVC	
SEQ ID NO:37	<u>M-----EDPDIKRCKL--SCVATVDDVIEQVMTYITDPKDRDSASLVC</u>	60
	<u>1</u>	
SEQ ID NO:18	-----	
SEQ ID NO:22	RRWYELDSLTRKHVTIALCYTTTPARLRRRFPHPHLESKLKGKPRAAFNLIPEDWGGHVT	
SEQ ID NO:20	RRWHRIDALTRKHVTVPFCYAAASPAHLARFPRLLES LAVKGKPRAA MYGLIPEDWGAYAR	
SEQ ID NO:37	<u>RRWFKIDSETREHVTMALCYTATPDRLSRFPNRLSLKKGKPRAAFNLIPEWGGYVT</u>	120
	<u>61</u>	
SEQ ID NO:18	-----	
SEQ ID NO:22	PWVKEISQYFDCLKSLHFRMIVKSDLQNLARDRGHVLHALKDKCSGFTTDDGLFHI	
SEQ ID NO:20	PWVAELAAPLECLKALHLRRMVVTDLALVRARGHMLQELKDKCSGFSTDALRLVAR	
SEQ ID NO:37	<u>PWVTEISNNLRQLKSVHFRMIVSDLDLRLAKARADDLETCLKDKCSGFTTDDGLLSIVT</u>	180
	<u>121</u>	
SEQ ID NO:18	-----	
SEQ ID NO:22	--RGLETLFLEESTIDEKENDEWIRELATSNSVLETNFFLTDL-RASPEYLTLLVRNCQ	
SEQ ID NO:20	FCKSLRVLFLEESSILEKD-GEWLHELALNNTVLETNLFYLTDIADV KIEDLELLAKNCP	
SEQ ID NO:20	SCRSLRTL FLEEC SIADNGT-EWLHDLAVNNPVLETNLFHMTTEL-TVVPADLELLAKKCK	
SEQ ID NO:37	<u>HCRKIKTLLMEESSFSEKD-GKWLHELQAQNTSLEVLNFYMTTEFAKISPKDLETIARNCR</u>	240
	<u>181</u>	

Figure 1B

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SEQ ID NO:18  RLKTLKISECFMPDLVSLFRTAQTQEFAGSFEEQGPVASRNYENYFFPPSLHRLSLL
SEQ ID NO:22  NLVSVKLTDCIILDVNFVKHASALEEFCGGTYNE--E---PERYSAISLPAKLCRLGLT
SEQ ID NO:20  SLISLKISDCDFSLDIGFFRMAASLQEFAGGAFIEQGELT---KYGNVKFP SRLCSLGLT
SEQ ID NO:37  SLVSVKVGDFEILELVGFFKAAANLEEFCCGSLNE--DIGMPEKYMNLVFP RKLCLRLGLS
                                     241
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
SEQ ID NO:18  YMGTNMQILFPYATALKKLDLQFTFLSTEDHCQIVQRCSNLETLEVRDVIGDRGLQVVA
SEQ ID NO:22  YIGKNELPIVFMFAAVLKKLDLLYAMLDTECHCLIQPCPNLEVLTRNVIGDRGLEVLG
SEQ ID NO:20  YMGTNEMPIIFPFSALLKKLDLQYFTLTEDHCQLIAKCPNLLVLAVRNVIGDRGLGVA
SEQ ID NO:37  YMGPNEMPILFPFAAQIRKLDLLYALLETECHCTLIQCPNLEVLTRNVIGDRGLEVLA
                                     301
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
SEQ ID NO:18  QTCCKLHLRLRVERGDDDDQGGLEDEQGRISQVGLMAIAQGCPELTYYWAIHVSDITNAALEA
SEQ ID NO:22  RCCKRLKRLRIERGDDDDQG-MEDEEGTVSHRGLIALSQGCSELEYMAVYVSDITNASLEH
SEQ ID NO:20  DTCKKLQRLRVERGDDDDPG-LQEEQGGVSQVGLTTVAVGCRELEYIAAYVSDITNGALES
SEQ ID NO:37  QYCKQLKRLRIERGADEQG-MEDEEGLVSQRGLIALAQGCQCELEYMAVYVSDITNESLES
                                     361
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
SEQ ID NO:18  VGTCCKNLNDFRLVLLDREAHITELPLDNGVRALLRGCTKLRRAFYVRPGALSDVGLGY
SEQ ID NO:22  IGTCLKNLCLDFRLVLLDHEEKITDPLDNGVRALLRGCDKLRRFALYLRGGGLTDVGLGY
SEQ ID NO:20  IGTFCCKNLCLDFRLVLLDREERITDPLDNGVRALLRGCTKLRRFALYLRPGGLSDTGLGY
SEQ ID NO:37  IGTCLKNLCLDFRLVLLDREERITDPLDNGVRSLIGCKKLRRAFYLRQGGGLTDLGLSY
                                     421

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Figure 1C

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SEQ ID NO:18 VGEFSKSIRYMLLGNVGESDNGIIQLSKGCPSLQKLEVRGC-LFSEHALALAAALQLKSLR ***
SEQ ID NO:22 IGQYSPNVRWMLLGYVGESDAGLLEFAKGCPSLQKLEMRGCLFFSERALAVAATQLTSLR ***
SEQ ID NO:20 IGQYSGIIQYMLLGNVGETDDGLIRFALGCENLRKLELRSC-CFSEQALARAIRSMPSLR ***
SEQ ID NO:37 IGQYSPNVRWMLLGYVGESDEGLMEFSRGCNPLQKLEMRGC-CFSERAIAAAATKLPCLR ***
481
***** * * * * * *****
SEQ ID NO:18 YLWVQGFRRSPTGTDIMAMVRPFWNIEYIVP-----DQDEPCPEHKRQILAYYSLA *****
SEQ ID NO:22 YLWVQGYGVSPSGRDLMLMARPFWNIELI-PSRKVATNTNPDETVVVEHPAHILAYYSLA *****
SEQ ID NO:20 YVWVQGYKASKTGHDLMMLMARPFWNIEFTPPSSENANRMREDGECVDSQAQILAYYSLA *****
SEQ ID NO:37 YLWVQGYRASMTGQDLMQMARPYWNIELI-PSRRVPEVNQQGEIREMEHPAHILAYYSLA *****
541
* * * * *
SEQ ID NO:18 GRTDCPPSVTLLYPAF-----
SEQ ID NO:22 GQRSDFPDTPVPLDTATCVDT
SEQ ID NO:20 GKRSDCPRSVVPLYP-----
SEQ ID NO:37 GQRTDCPTTVRVLKEPI-----
601
621

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Figure 2A

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***
SEQ ID NO: 30 MPVMAPTASL---LLSPRPLPASRRVPSPSPA-----LSASGRLRLRRARADTRLRVA
SEQ ID NO: 32 MALPHSISALATTLTLSSPITKPHKVNPFPFSSNRNSQFLTQTRPRSRRLNLSLTPARVA
SEQ ID NO: 36 -----LRVA
SEQ ID NO: 38 MRATIPALS L---LVTPR-----LPSLAV-----PLAGGRLR-EGGRSRTRLRVA
1 60

** *
SEQ ID NO: 30 APPSVPG EAD--QAPGETEPSTSSAD---EKFVWRDHWYPVSVLVEDLDPSVPTPFQLLNR
SEQ ID NO: 32 APPSTVEADRLYPEAENNETEEEEFSDESSKFTWRDHWYPVSLIEDLNPLLPFPQLLGR
SEQ ID NO: 36 APTSVPG EAE--RAEEPSTSTSPESSEKGFVWRDHWYPVSVLVEDLDPRVPTPFQLLNR
SEQ ID NO: 38 APTSVPG EAA--EQAEPTSAPES----GEKFSWRDHWYPVSVLVEDLDPSRPTPFQLLNR
61 120

* *
SEQ ID NO: 30 DLVIWKDPKSGEWVALDDRCPHRLAPLSEGRIDETGCLQCSYHGWSFDGSGACTRIPQAA
SEQ ID NO: 32 EIVLWYDKSISQWVAFDDKCPHRLAPLSEGRIDEDGKLQCSYHGWSFDGCGCVKIPQAS
SEQ ID NO: 36 DLVIWNDPNSGDWVALDDRCPHRLAPLSEGRIDETGGLQCSYHGWSFDGSGACTRIPQAA
SEQ ID NO: 38 DLVIWKEPKSGEWVALDDRCPHRLAPLSEGRIDETGCLQCSYHGWSFDGSGACTKIPQAM
121 180

***** *
SEQ ID NO: 30 PEGPEAKAVRSPKACAIFFTLLVSQGLLFVWPDENGW EKATATKPPMLPKEFEDPAFSTV
SEQ ID NO: 32 SEGPEARAIGSPKACATRFPTLLVSQGLLFVWADENGW EKAKASNPPMPDDEFKPEFFPTV
SEQ ID NO: 36 PEGPEARAVRSPKACATKFTPTLLSQGLLFVWPDENGW DKAKATKPPMLPKEFDDPAFSTV
SEQ ID NO: 38 PEGPEARAVRSPKACAIFFTLLVSQGLLFVWPDENGW EKAATAKPPMLPKEFEDPAFSTV
181 240
```

Figure 2B

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*****
SEQ ID NO:30  TIQRDLYYGYDTLMENVSDPSHIEFAHXHKVTGRRDRARPLPFKMESSGAWGYSGNSGNP
SEQ ID NO:32  NIQRDLFYGYDTLMENVSDPSHIEFAHHKVTGRRDRAKPLPFKMDSRGSGWGFSGANEGNP
SEQ ID NO:36  TIQRDLFYGYDTLMENVSDPSHIEFAHHKVTGRRDRAKPLPFKMESSGAWGYSGANTGNP
SEQ ID NO:38  TIQRDLFYGYDTLMENVSDPSHIEFAHHKVTGRRDRARPLTFRMESSGAWGYSGANSNP
                                     300
                                     241

*****
SEQ ID NO:30  RISATFVAPCYALNKIEIDTKLPIFGDQKWVIWICSFNIPMAPGKTRSIVCARNFFQFS
SEQ ID NO:32  QISAKFVAPCYMMNKIEIDTKLPVVGDKWVWICSFNVPAPGKTRSIVCARNFFQFS
SEQ ID NO:36  RITATFEAPCYALNKIEIDTKLPIVGDKWVIWICSFNIPMAPGKTRSIVCARNFFQFT
SEQ ID NO:38  RITATFEAPCYALNKIEIDTKLPIFGDQKWVIWICSFNIPMAPGKTRSIVCARNFFQFT
                                     360
                                     301

*****
SEQ ID NO:30  MPGKAWWQL-----VPRWYEHWTSNLVYDGMIVLQGQEKIFLSAS
SEQ ID NO:32  VPGPAWWQVNVILLFAFNFKQCIHVTQVVPRWYEHWTSNKVYDGMIVLQGQEKIFLSET
SEQ ID NO:36  MPGKAWWQF-----VPRWYEHWTSNLVYDGMIVLQGQEKVFLSAS
SEQ ID NO:38  MPGKAWWQL-----VPRWYEHWTSNLVYDGMIVLQGQEKIFLAAT
                                     420
                                     361

*****
SEQ ID NO:30  KESSADINQQYTKITFTPTQADRFVLAFAWLRFKFGNSQPDWFNGNPSQEVLPSTVLSKRE
SEQ ID NO:32  KEGG-DINKQYTNITFTPTQADRFVLAFRNLRRHNGNQPEWFGNSSDQPLPSTVLSKRQ
SEQ ID NO:36  KESSADVNNQQYTKLFTFTPTQADRFVLAFAWLRFKFGNSQPDWYGSPSQDALPSTVLSKRE
SEQ ID NO:38  KESSTDINQQYTKITFTPTQADRFVLAACRTWLRFKFGNSQPEWFGNPTQEALPSTVLSKRE
                                     480
                                     421

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Figure 2C

SEQ ID NO: 30	MLDRYEQTTLKCSSCKGAYNAFQTLQKVMGATVA-----VLLLL-----	481
SEQ ID NO: 32	MLDRFEQHTLKCSSCKAAYEGFQTWQKVLIGATVVFCAATSGIPSDFQLRVLLAGLAVVSA	
SEQ ID NO: 36	MLDRYEQHTLKCSSCKRGAHKAFTLQKVMGATVVFCAATSGIPADVQLRILLGAGALVSA	
SEQ ID NO: 38	MLDRYEQLSLKCSSCKGAYNAFQNLQKVMGATVVCCAAAGIPPDVQLRLLIGAAALVSA	540
SEQ ID NO: 30	-----	
SEQ ID NO: 32	AIAFALNQLQKNFEFVDYVHAEID	
SEQ ID NO: 36	ALAYVFYDRQKHFFVVDYVHADID	
SEQ ID NO: 38	AIAYAFHELQKNFVVDYVHADID	541
		564